

## SEQUENCE LISTING

<110> Aventis Pasteur Limited  
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 Murdin, Andrew

<120> Chlamydia mgp002

<130> APL-03-03-PCT

<150> 60/481,690

<151> 2003-11-21

<160> 14

<170> PatentIn version 3.3

<210> 1

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<212> DNA

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Lys Ser Ala Ile Ile Gly Ala Gly Leu Ser Gly Ser Ser Glu Thr Leu	
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Asp Leu Leu Ser Glu Ser Ile Glu Thr Gln Asp Leu Tyr Glu Gln Leu	
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Ile	Leu	Ser	Ser	Leu	Leu	Lys	Leu	Pro	Asn	Asn	Ala	Tyr	Leu	Pro	Tyr	
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Thr	Leu	Val	Ser	Ser	Lys	Thr	Asp	Glu	Asp	Ile	Arg	Val	Phe	Leu	Ser	
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gat gct gaa aat ccg ctt ccc tct cca agc tct tct tat tta cgc tac 1536  
 Asp Ala Glu Asn Pro Leu Pro Ser Pro Ser Ser Ser Tyr Leu Arg Tyr  
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caa gta tcc cct gag acc cgc aca caa ctt atg cta gct att ttg gaa 1584  
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 515 520 525

acc tta gtt tct tcc aaa acg gat gaa gat atc cgc gtt ttt ctt tcc 1632  
 Thr Leu Val Ser Ser Lys Thr Asp Glu Asp Ile Arg Val Phe Leu Ser  
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Ser Cys Arg Lys Ser Val Pro Gln Ala Leu Glu Ala Tyr Leu Glu Ala  
 35 40 45

Ser Ala Thr Tyr Gln Gln His Asp Phe Ser Val Leu Arg Val Ile Ala  
 50 55 60

Glu Ser Tyr Leu Gln Gln Ser Phe Leu Ser Glu Asp Thr Tyr Ile Arg  
 65 70 75 80

Lys Ser Ala Ile Ile Gly Ala Gly Leu Ser Gly Ser Ser Glu Ala Leu  
 85 90 95

Glu Leu Leu Ser Glu Ala Ile Glu Thr Gln Asp Leu Tyr Glu Gln Leu  
 100 105 110

Leu Ile Leu Asn Ala Ala Thr Ser Gln Leu Ser Lys Thr Ser Asp Lys  
 115 120 125

Leu Leu Phe Lys Gly Leu Thr Ala Ser His Pro Val Ile Arg Leu Glu  
 130 135 140

Ala Ala Tyr Arg Leu Ala Cys Met Lys Asn Ser Lys Val Ser Asp Tyr  
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 165 170 175

Ala Thr Ile Phe Leu Gln Leu Glu Thr Glu Glu Ala Asp Ala Tyr Ile  
 180 185 190

His His Leu Leu Ser Ser Pro Asn Asn Leu Thr Arg Asn Tyr Val Ala  
 195 200 205

Tyr Leu Ile Gly Glu Tyr Lys Gln Lys Arg Phe Leu Pro Thr Leu Arg  
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Ser Leu Leu Thr Ser Ala Ser Pro Leu Asp Gln Glu Gly Ala Leu Tyr  
 225 230 235 240

Ala Leu Gly Lys Leu Glu Asp Ser Gly Ser Tyr Pro Arg Ile Lys Ala  
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Leu Ser Ser Arg Ser Asn Pro Glu Val Val Leu Ala Ala Ala Gln Thr  
 260 265 270

Leu Leu Phe Leu Glu Lys Glu Glu Glu Ala Leu Pro Ile Leu Thr Asn  
 275 280 285

Leu Cys Gln Gln Lys Leu Leu Arg Ala Leu Tyr Thr Ala Arg Phe Leu  
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Ser Gln Glu Lys Gly Glu Glu Leu Leu Leu Pro Ile Phe Tyr Asn Ala  
 305 310 315 320

325

330

335

Gly Cys Thr Asp Pro Gln Val Leu His Tyr Leu Thr Glu Ile Leu Glu  
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Ser Lys Val Leu His Arg Ile Phe Leu Pro Thr His Ser Thr Gly Lys  
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Ala Ile Gln Phe Trp Lys Glu Cys Thr Thr Phe Pro Leu Met Ser Gln  
 370 375 380

Glu Asp Lys Met Arg Thr Leu Ala Met Tyr Arg Val Ala Glu Asp Thr  
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Ile Leu Ser Ala Leu Leu Lys Leu Pro Asn Asp Ala Tyr Leu Pro Tyr  
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Leu Tyr Arg Tyr Ala Glu Gln Leu Ile Glu Asp Thr Ile Leu Phe Thr  
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Gln Val Ser Pro Glu Thr Arg Thr Gln Leu Met Leu Ala Ile Leu Glu  
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&lt;210&gt; 5

&lt;211&gt; 1695

&lt;212&gt; DNA

&lt;213&gt; Chlamydia muridarum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1695)

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acc tat caa caa cat aac ttt tct ata ttg cgc tta ata gct aag tca 144  
Thr Tyr Gln Gln His Asn Phe Ser Ile Leu Arg Leu Ile Ala Lys Ser

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120

125

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	180	185	190	
att gga gaa tat caa cag agg aga ttt ctt cca acg ctc cgc tcg ttg				624
Ile Gly Glu Tyr Gln Gln Arg Arg Phe Leu Pro Thr Leu Arg Ser Leu				
	195	200	205	
ctt acc agc gca gct cct tta gac caa gaa gga tct ttg tat gct ata				672
Leu Thr Ser Ala Ala Pro Leu Asp Gln Glu Gly Ser Leu Tyr Ala Ile				
	210	215	220	
gga aaa tta gaa gat gcc agc agc tat cct aaa atc aaa gca tta agc				720
Gly Lys Leu Glu Asp Ala Ser Ser Tyr Pro Lys Ile Lys Ala Leu Ser				
	225	230	235	240
tcc aaa tct aac cct gaa gtg gct ctt gct gct gct cag aca tta tta				768
Ser Lys Ser Asn Pro Glu Val Ala Leu Ala Ala Ala Gln Thr Leu Leu				
	245	250	255	
ttc ttg ggt aaa gaa gat gag gct ctt cct atc cta act act ttt tgc				816
Phe Leu Gly Lys Glu Asp Glu Ala Leu Pro Ile Leu Thr Thr Phe Cys				
	260	265	270	
cag caa gag ctt cct cga gct att tat acc tct cgt ttc ctt tca tta				864
Gln Gln Glu Leu Pro Arg Ala Ile Tyr Thr Ser Arg Phe Leu Ser Leu				
	275	280	285	
gaa aaa gga gaa gag ctt ctt tta ccc atc ttt tgt aaa gct att aaa				912
Glu Lys Gly Glu Glu Leu Leu Leu Pro Ile Phe Cys Lys Ala Ile Lys				
	290	295	300	
gaa gaa att aaa ctg aat gct gct ttg gct ctt gtc cac ttg gga agc				960
Glu Glu Ile Lys Leu Asn Ala Ala Leu Ala Leu Val His Leu Gly Ser				
	305	310	315	320
gtt aat cac cta gtg ctt agt tat tta aca gaa ttt tta gaa aat aaa				1008
Val Asn His Leu Val Leu Ser Tyr Leu Thr Glu Phe Leu Glu Asn Lys				
	325	330	335	
att ctc cac cgc ata ttt tta ccc acc cat tcg ata gga aaa gcc acg				1056
Ile Leu His Arg Ile Phe Leu Pro Thr His Ser Ile Gly Lys Ala Thr				
	340	345	350	
cag ttt tgg aaa gag tgt acg gca ctc cct ctt cta agc cca gaa gaa				1104
Gln Phe Trp Lys Glu Cys Thr Ala Leu Pro Leu Leu Ser Pro Glu Glu				
	355	360	365	
aaa gca aga gct ttg gca atg tat cgc gca gca gaa gat acg atc ctc				1152

370	375	380	
tct agt tta tta aaa tta cct aac aat gcc tat ctg cct tat ttg gaa Ser Ser Leu Leu Lys Leu Pro Asn Asn Ala Tyr Leu Pro Tyr Leu Glu 385 390 395 400			1200
cgt att cta act tca caa aaa acc cct cta gca gct aaa gct att gct Arg Ile Leu Thr Ser Gln Lys Thr Pro Leu Ala Ala Lys Ala Ile Ala 405 410 415			1248
ttt tta tca gta aca gct cat cct cag gca ctt tct tta gtc tcg aaa Phe Leu Ser Val Thr Ala His Pro Gln Ala Leu Ser Leu Val Ser Lys 420 425 430			1296
gca gca cta act cca gga gac cct atc att cgc gct tat gcg aat tta Ala Ala Leu Thr Pro Gly Asp Pro Ile Ile Arg Ala Tyr Ala Asn Leu 435 440 445			1344
gct tta tat aca atg acg caa gat cct gaa aag aaa gcc tta tta tat Ala Leu Tyr Thr Met Thr Gln Asp Pro Glu Lys Lys Ala Leu Leu Tyr 450 455 460			1392
caa tat gcc gaa cag tta ata gga gac acg att ttg ttt aca gat gag Gln Tyr Ala Glu Gln Leu Ile Gly Asp Thr Ile Leu Phe Thr Asp Glu 465 470 475 480			1440
gag aat ccc ctg cct tct ccc cat tct tcc tac ctg cga tat caa gtg Glu Asn Pro Leu Pro Ser Pro His Ser Ser Tyr Leu Arg Tyr Gln Val 485 490 495			1488
tcc cca gaa act cgt tct caa ctc atg cta act att tta gaa acc cta Ser Pro Glu Thr Arg Ser Gln Leu Met Leu Thr Ile Leu Glu Thr Leu 500 505 510			1536
gtt tct tct aaa act gat gaa gac atc cga gtt ttt ctt tcg cta atg Val Ser Ser Lys Thr Asp Glu Asp Ile Arg Val Phe Leu Ser Leu Met 515 520 525			1584
aaa aaa acc cat tac aaa aat atc ccc atc tta tct gga tta tta atg Lys Lys Thr His Tyr Lys Asn Ile Pro Ile Leu Ser Gly Leu Leu Met 530 535 540			1632
aga ata gtg gag cga gct cgg tac caa gct tac gta gaa caa aaa ctc Arg Ile Val Glu Arg Ala Arg Tyr Gln Ala Tyr Val Glu Gln Lys Leu 545 550 555 560			1680
atc tca gaa gag gat Ile Ser Glu Glu Asp 565			1695

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&lt;211&gt; 565

&lt;212&gt; PRT

&lt;213&gt; Chlamydia muridarum

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 Gln Lys Ser Ile Pro Gln Ala Leu Glu Ser Tyr Leu Glu Ala Ser Thr  
 20 25 30  
 Thr Tyr Gln Gln His Asn Phe Ser Ile Leu Arg Leu Ile Ala Lys Ser  
 35 40 45  
 Tyr Leu Gln Gln Ser Leu Phe Ser Glu Asp Ala Tyr Val Arg Lys Ser  
 50 55 60  
 Ala Ile Ile Gly Ala Gly Leu Ser Gly Ser Ser Glu Thr Leu Asp Leu  
 65 70 75 80  
 Leu Ser Glu Ser Ile Glu Thr Gln Asp Leu Tyr Glu Gln Leu Leu Ile  
 85 90 95  
 Leu Asn Ala Ala Gly Asn Gln Leu Gly Lys Thr Ser Asp Arg Leu Leu  
 100 105 110  
 Phe Lys Gly Leu Thr Ala Pro His Pro Ile Ile Arg Leu Glu Ala Ala  
 115 120 125  
 Tyr Arg Leu Ala Cys Met Lys Asn Ser Lys Val Ser Asp Tyr Leu Tyr  
 130 135 140  
 Ser Phe Ile His Gln Leu Pro Glu Glu Ile Gln Asn Leu Ala Ala Thr  
 145 150 155 160  
 Ile Phe Leu Gln Leu Glu Thr Glu Glu Ala Asp Ala Tyr Val His Arg  
 165 170 175  
 Leu Leu Ser Ser Pro Asn Ser Leu Thr Arg Asn Tyr Met Ala Tyr Leu  
 180 185 190  
 Ile Gly Glu Tyr Gln Gln Arg Arg Phe Leu Pro Thr Leu Arg Ser Leu  
 195 200 205  
 Leu Thr Ser Ala Ala Pro Leu Asp Gln Glu Gly Ser Leu Tyr Ala Ile  
 210 215 220

Gly Lys Leu Glu Asp Ala Ser Ser Tyr Pro Lys Ile Lys Ala Leu Ser  
 225 230 235 240

Ser Lys Ser Asn Pro Glu Val Ala Leu Ala Ala Ala Gln Thr Leu Leu  
 245 250 255

Phe Leu Gly Lys Glu Asp Glu Ala Leu Pro Ile Leu Thr Thr Phe Cys  
 260 265 270

Gln Gln Glu Leu Pro Arg Ala Ile Tyr Thr Ser Arg Phe Leu Ser Leu  
 275 280 285

Glu Lys Gly Glu Glu Leu Leu Leu Pro Ile Phe Cys Lys Ala Ile Lys  
 290 295 300

Glu Glu Ile Lys Leu Asn Ala Ala Leu Ala Leu Val His Leu Gly Ser  
 305 310 315 320

Val Asn His Leu Val Leu Ser Tyr Leu Thr Glu Phe Leu Glu Asn Lys  
 325 330 335

Ile Leu His Arg Ile Phe Leu Pro Thr His Ser Ile Gly Lys Ala Thr  
 340 345 350

Gln Phe Trp Lys Glu Cys Thr Ala Leu Pro Leu Leu Ser Pro Glu Glu  
 355 360 365

Lys Ala Arg Ala Leu Ala Met Tyr Arg Ala Ala Glu Asp Thr Ile Leu  
 370 375 380

Ser Ser Leu Leu Lys Leu Pro Asn Asn Ala Tyr Leu Pro Tyr Leu Glu  
 385 390 395 400

Arg Ile Leu Thr Ser Gln Lys Thr Pro Leu Ala Ala Lys Ala Ile Ala  
 405 410 415

Phe Leu Ser Val Thr Ala His Pro Gln Ala Leu Ser Leu Val Ser Lys  
 420 425 430

Ala Ala Leu Thr Pro Gly Asp Pro Ile Ile Arg Ala Tyr Ala Asn Leu  
 435 440 445



Ala Leu Tyr Thr Met Thr Gln Asp Pro Glu Lys Lys Ala Leu Leu Tyr  
450 455 460

Gln Tyr Ala Glu Gln Leu Ile Gly Asp Thr Ile Leu Phe Thr Asp Glu  
465 470 475 480

Glu Asn Pro Leu Pro Ser Pro His Ser Ser Tyr Leu Arg Tyr Gln Val  
485 490 495

Ser Pro Glu Thr Arg Ser Gln Leu Met Leu Thr Ile Leu Glu Thr Leu  
500 505 510

Val Ser Ser Lys Thr Asp Glu Asp Ile Arg Val Phe Leu Ser Leu Met  
515 520 525

Lys Lys Thr His Tyr Lys Asn Ile Pro Ile Leu Ser Gly Leu Leu Met  
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Arg Ile Val Glu Arg Ala Arg Tyr Gln Ala Tyr Val Glu Gln Lys Leu  
545 550 555 560

Ile Ser Glu Glu Asp  
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cga aaa tca gtc cct caa gct cta gaa gcc tat ctc gaa gct tca gca 96  
Arg Lys Ser Val Pro Gln Ala Leu Glu Ala Tyr Leu Glu Ala Ser Ala  
20 25 30

act tat caa caa cac gat ttc tcc gta tta cgc gta ata gca gaa tcg 144  
Thr Tyr Gln Gln His Asp Phe Ser Val Leu Arg Val Ile Ala Glu Ser  
35 40 45

Tyr	Leu	Gln	Gln	Ser	Phe	Leu	Ser	Glu	Asp	Thr	Tyr	Ile	Arg	Lys	Ser		
50						55					60						
gca	att	att	gga	gca	ggg	cta	tct	ggt	tca	tca	gaa	gct	tta	gag	tta	240	
Ala	Ile	Ile	Gly	Ala	Gly	Leu	Ser	Gly	Ser	Ser	Glu	Ala	Leu	Glu	Leu		
65					70				75					80			
ctg	tct	gag	gct	ata	gaa	acg	caa	gat	ctc	tat	gag	caa	cta	ctc	att	288	
Leu	Ser	Glu	Ala	Ile	Glu	Thr	Gln	Asp	Leu	Tyr	Glu	Gln	Leu	Leu	Ile		
				85					90					95			
tta	aat	gct	gca	acc	agc	caa	tta	agc	aaa	act	tct	gac	aaa	ctt	tta	336	
Leu	Asn	Ala	Ala	Thr	Ser	Gln	Leu	Ser	Lys	Thr	Ser	Asp	Lys	Leu	Leu		
			100					105					110				
ttc	aag	gga	tta	aca	gct	tct	cat	cct	gtc	atc	cgc	tta	gaa	gct	gct	384	
Phe	Lys	Gly	Leu	Thr	Ala	Ser	His	Pro	Val	Ile	Arg	Leu	Glu	Ala	Ala		
		115					120						125				
tat	cgt	ctt	gcc	tgt	atg	aaa	aat	agc	aag	gta	agt	gat	tac	ctt	tat	432	
Tyr	Arg	Leu	Ala	Cys	Met	Lys	Asn	Ser	Lys	Val	Ser	Asp	Tyr	Leu	Tyr		
	130					135					140						
tct	ttt	atc	tac	aag	tta	cca	gaa	gaa	att	caa	aac	cta	gcg	gca	act	480	
Ser	Phe	Ile	Tyr	Lys	Leu	Pro	Glu	Glu	Ile	Gln	Asn	Leu	Ala	Ala	Thr		
145					150					155					160		
att	ttc	tta	caa	ctc	gaa	aca	gaa	gaa	gct	gat	gct	tat	att	cat	cat	528	
Ile	Phe	Leu	Gln	Leu	Glu	Thr	Glu	Glu	Ala	Asp	Ala	Tyr	Ile	His	His		
				165					170					175			
ttg	ctc	tct	tct	ccc	aat	aac	ctg	aca	aga	aac	tat	gtt	gcc	tat	tta	576	
Leu	Leu	Ser	Ser	Pro	Asn	Asn	Leu	Thr	Arg	Asn	Tyr	Val	Ala	Tyr	Leu		
			180					185					190				
att	gga	gag	tac	aaa	caa	aaa	aga	ttt	ctt	cca	aca	cta	cgc	tct	tta	624	
Ile	Gly	Glu	Tyr	Lys	Gln	Lys	Arg	Phe	Leu	Pro	Thr	Leu	Arg	Ser	Leu		
		195					200					205					
ctt	aca	agt	gcc	tct	cct	tta	gat	caa	gaa	ggc	gct	ttg	tat	gcg	tta	672	
Leu	Thr	Ser	Ala	Ser	Pro	Leu	Asp	Gln	Glu	Gly	Ala	Leu	Tyr	Ala	Leu		
	210				215					220							
ggc	aaa	ctg	gaa	gac	tct	ggt	agc	tat	cct	aga	att	aaa	gct	cta	agc	720	
Gly	Lys	Leu	Glu	Asp	Ser	Gly	Ser	Tyr	Pro	Arg	Ile	Lys	Ala	Leu	Ser		
225				230					235					240			
tct	aga	tcc	aat	cct	gaa	gta	gta	ctc	gct	gca	gct	cag	aca	tta	tta	768	
Ser	Arg	Ser	Asn	Pro	Glu	Val	Val	Leu	Ala	Ala	Ala	Gln	Thr	Leu	Leu		
				245				250						255			
ttc	tta	gag	aaa	gaa	gaa	gaa	gct	cta	ccg	atc	cta	acc	aac	ctt	tgc	816	
Phe	Leu	Glu	Lys	Glu	Glu	Glu	Ala	Leu	Pro	Ile	Leu	Thr	Asn	Leu	Cys		
			260				265						270				
caa	caa	aaa	ctt	ctt	cga	gcc	ctg	tat	acc	gca	cgt	ttc	ctc	tcg	caa	864	

275	280	285	
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gaa gaa att aga ctg aat act gct tta gca ctt gtt cat caa ggg tgt Glu Glu Ile Arg Leu Asn Thr Ala Leu Ala Leu Val His Gln Gly Cys 305 310 315 320			960
aca gat cct caa gtc ctc cac tat cta aca gaa atc tta gaa agt aaa Thr Asp Pro Gln Val Leu His Tyr Leu Thr Glu Ile Leu Glu Ser Lys 325 330 335			1008
gtt ctc cat cgc ata ttt tta cct act cac tcg aca gga aaa gct ata Val Leu His Arg Ile Phe Leu Pro Thr His Ser Thr Gly Lys Ala Ile 340 345 350			1056
cag ttc tgg aaa gaa tgc acc act ttt cct ctc atg agc caa gaa gac Gln Phe Trp Lys Glu Cys Thr Thr Phe Pro Leu Met Ser Gln Glu Asp 355 360 365			1104
aaa atg aga acg ttg gct atg tat cgg gta gcg gaa gat acc atc ctc Lys Met Arg Thr Leu Ala Met Tyr Arg Val Ala Glu Asp Thr Ile Leu 370 375 380			1152
tca gcg tta cta aaa tta ccc aat gac gcc tat ctt cct tac cta gag Ser Ala Leu Leu Lys Leu Pro Asn Asp Ala Tyr Leu Pro Tyr Leu Glu 385 390 395 400			1200
cgc atc ctc gcc tca caa aaa act ata cta gca gct aaa gct att gct Arg Ile Leu Ala Ser Gln Lys Thr Ile Leu Ala Ala Lys Ala Ile Ala 405 410 415			1248
ttt tta tcg gta aca gct cat cct cag gca ctt tct tta gtc tcg aaa Phe Leu Ser Val Thr Ala His Pro Gln Ala Leu Ser Leu Val Ser Lys 420 425 430			1296
gct gca tta act cct gga gac cct atc att cgc gct tac gct aat cta Ala Ala Leu Thr Pro Gly Asp Pro Ile Ile Arg Ala Tyr Ala Asn Leu 435 440 445			1344
gct tta tat aca atg acc aaa gat cct gag aaa aaa gct gtg cta tac Ala Leu Tyr Thr Met Thr Lys Asp Pro Glu Lys Lys Ala Val Leu Tyr 450 455 460			1392
cga tat gct gaa caa tta ata gag gat acc att tta ttc aca gat gct Arg Tyr Ala Glu Gln Leu Ile Glu Asp Thr Ile Leu Phe Thr Asp Ala 465 470 475 480			1440
gaa aat ccg ctt ccc tct cca agc tct tct tat tta cgc tac caa gta Glu Asn Pro Leu Pro Ser Pro Ser Ser Tyr Leu Arg Tyr Gln Val 485 490 495			1488
tcc cct gag acc cgc aca caa ctt atg cta gct att ttg gaa acc tta Ser Pro Glu Thr Arg Thr Gln Leu Met Leu Ala Ile Leu Glu Thr Leu 500 505 510 515 520			1536

gtt tct tcc aaa acg gat gaa gat atc cgc gtt ttt ctt tcc cta atg 1584  
 Val Ser Ser Lys Thr Asp Glu Asp Ile Arg Val Phe Leu Ser Leu Met  
           515                               520                               525

aaa aaa acc cat tac aaa aat atc ccg atc tta tca gga ttg tta atg 1632  
 Lys Lys Thr His Tyr Lys Asn Ile Pro Ile Leu Ser Gly Leu Leu Met  
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aga ata gtg gag 1644  
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<213> Chlamydia trachomatis

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Arg Lys Ser Val Pro Gln Ala Leu Glu Ala Tyr Leu Glu Ala Ser Ala  
           20                               25                               30

Thr Tyr Gln Gln His Asp Phe Ser Val Leu Arg Val Ile Ala Glu Ser  
           35                               40                               45

Tyr Leu Gln Gln Ser Phe Leu Ser Glu Asp Thr Tyr Ile Arg Lys Ser  
           50                               55                               60

Ala Ile Ile Gly Ala Gly Leu Ser Gly Ser Ser Glu Ala Leu Glu Leu  
 65                               70                               75                               80

Leu Ser Glu Ala Ile Glu Thr Gln Asp Leu Tyr Glu Gln Leu Leu Ile  
           85                               90                               95

Leu Asn Ala Ala Thr Ser Gln Leu Ser Lys Thr Ser Asp Lys Leu Leu  
           100                               105                               110

Phe Lys Gly Leu Thr Ala Ser His Pro Val Ile Arg Leu Glu Ala Ala  
           115                               120                               125

Tyr Arg Leu Ala Cys Met Lys Asn Ser Lys Val Ser Asp Tyr Leu Tyr  
           130                               135                               140

Ser Phe Ile Tyr Lys Leu Pro Glu Glu Ile Gln Asn Leu Ala Ala Thr  
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Ile Phe Leu Gln Leu Glu Thr Glu Glu Ala Asp Ala Tyr Ile His His  
 165 170 175

Leu Leu Ser Ser Pro Asn Asn Leu Thr Arg Asn Tyr Val Ala Tyr Leu  
 180 185 190

Ile Gly Glu Tyr Lys Gln Lys Arg Phe Leu Pro Thr Leu Arg Ser Leu  
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Leu Thr Ser Ala Ser Pro Leu Asp Gln Glu Gly Ala Leu Tyr Ala Leu  
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Gly Lys Leu Glu Asp Ser Gly Ser Tyr Pro Arg Ile Lys Ala Leu Ser  
 225 230 235 240

Ser Arg Ser Asn Pro Glu Val Val Leu Ala Ala Ala Gln Thr Leu Leu  
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Phe Leu Glu Lys Glu Glu Glu Ala Leu Pro Ile Leu Thr Asn Leu Cys  
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Gln Gln Lys Leu Leu Arg Ala Leu Tyr Thr Ala Arg Phe Leu Ser Gln  
 275 280 285

Glu Lys Gly Glu Glu Leu Leu Leu Pro Ile Phe Tyr Asn Ala Thr Gln  
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Glu Glu Ile Arg Leu Asn Thr Ala Leu Ala Leu Val His Gln Gly Cys  
 305 310 315 320

Thr Asp Pro Gln Val Leu His Tyr Leu Thr Glu Ile Leu Glu Ser Lys  
 325 330 335

Val Leu His Arg Ile Phe Leu Pro Thr His Ser Thr Gly Lys Ala Ile  
 340 345 350

Gln Phe Trp Lys Glu Cys Thr Thr Phe Pro Leu Met Ser Gln Glu Asp  
 355 360 365

370                      375                      380  
 Ser Ala Leu Leu Lys Leu Pro Asn Asp Ala Tyr Leu Pro Tyr Leu Glu  
 385                      390                      395                      400  
 Arg Ile Leu Ala Ser Gln Lys Thr Ile Leu Ala Ala Lys Ala Ile Ala  
                     405                      410                      415  
 Phe Leu Ser Val Thr Ala His Pro Gln Ala Leu Ser Leu Val Ser Lys  
                     420                      425                      430  
 Ala Ala Leu Thr Pro Gly Asp Pro Ile Ile Arg Ala Tyr Ala Asn Leu  
                     435                      440                      445  
 Ala Leu Tyr Thr Met Thr Lys Asp Pro Glu Lys Lys Ala Val Leu Tyr  
                     450                      455                      460  
 Arg Tyr Ala Glu Gln Leu Ile Glu Asp Thr Ile Leu Phe Thr Asp Ala  
 465                      470                      475                      480  
 Glu Asn Pro Leu Pro Ser Pro Ser Ser Ser Tyr Leu Arg Tyr Gln Val  
                     485                      490                      495  
 Ser Pro Glu Thr Arg Thr Gln Leu Met Leu Ala Ile Leu Glu Thr Leu  
                     500                      505                      510  
 Val Ser Ser Lys Thr Asp Glu Asp Ile Arg Val Phe Leu Ser Leu Met  
                     515                      520                      525  
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